

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:59:57 ; Search time 39 Seconds  
(without alignments)  
61.625 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	101	73.2	271	2 S29239	chymotrypsin (EC 3
2	94	68.1	265	2 T10495	chymotrypsin (EC 3
3	91	65.9	31	2 S61558	chymotrypsin Pml -
4	89	64.5	226	1 KCUF	bradyrin (EC 3.4
5	80	58.0	31	2 S18356	chymotrypsin (EC 3
6	74	53.6	309	2 B49878	coagulation factor
7	71	51.4	20	2 A56900	chymotrypsin I (EC
8	69	50.0	271	2 A25528	pancreatic elastase
9	69	50.0	460	2 B61545	plasmin (EC 3.4.21
10	69	50.0	1524	2 T30337	polyprotein - Afri
11	68	49.3	25	2 A23698	trypsin (EC 3.4.2
12	67	48.6	23	2 P00036	serine proteinase
13	67	48.6	244	2 S72219	chymotrypsin B - A
14	67	48.6	268	2 S68826	pancreatic elastase
15	67	48.6	268	2 S68825	pancreatic elastase
16	66	47.8	271	1 ELRT2	pancreatic elastase
17	65	47.1	262	1 A31372	granzyme A (EC 3.4
18	64	46.4	269	2 B26823	pancreatic elastase
19	63	45.7	20	2 A34817	collagenolytic pro
20	63	45.7	269	2 A26823	pancreatic elastase
21	63	45.7	273	2 A47246	trypsin (EC 3.4.2
22	63	45.7	274	2 A45754	trypsin (EC 3.4.2
23	63	45.7	275	2 C35863	trypsin (EC 3.4.2
24	63	45.7	812	1 PLMS	plasmin (EC 3.4.21
25	63	45.7	812	1 PLBO	apolipoprotein(a)
26	63	45.7	1420	2 A32869	apolipoprotein(a)
27	62	45.7	4548	1 S00657	alkaline trypsin-1
28	62	44.9	24	2 P00657	hypothetical prote
29	62	44.9	331	2 T27906	

plasmin (EC 3.4.21)  
plasmin (EC 3.4.21)  
enteropeptidase (E  
mast cell tryptase  
plasmin (EC 3.4.21)  
neutropsin - mouse  
tissue kallikrein  
cathepsin G (EC 3.  
chymotrypsin (EC 3  
pancreatic elastase  
plasmin (EC 3.4.21)  
tissue kallikrein  
mastocytoma proteol  
r-kininogenase (EC  
pancreatic elastase  
chymotrypsin (EC 3

## ALIGNMENTS

### RESULT 1

S29239  
chymotrypsin (EC 3.4.21.1) 1 precursor - penaeid shrimp (Penaeus vanamei)  
C:Species: Penaeus vanamei  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 22-Jun-1999  
C:Accession: S29239; S22075  
R:Sellos, D.; van Wormhoudt, A.  
FEBS Lett. 309, 219-224, 1992  
A:Title: Molecular cloning of a cDNA that encodes a serine protease with chymotryptic  
A:Reference number: S29239; MUID:92387359; PMID:1516690  
A:Accession: S29239  
A:Molecule type: mRNA  
A:Residues: 1-271 <SEL>  
A:Cross-references: EMBL:X66415; NID:g10088; PIDN:CAA47046.1; PID:g10089  
A:Note: the authors did not translate the codon for residue 1  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-271/Product: chymotrypsin 1 #status predicted <SIG>  
F:46-263/Domain: trypsin homology <TRY>  
F:86,132,223/Active site: His, Asp, Ser #status predicted

Query Match 73.2%; Score 101; DB 2; Length 271;  
Best Local Similarity 72.0%; Pred. No. 7.4e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
Db 46 IVGGVEATPHSWPQAALFIDDMYF 70  
|||||  
|||||

### RESULT 2

T10495  
chymotrypsin (EC 3.4.21.1) BII - penaeid shrimp (Penaeus vanamei) (fragment)  
C:Species: Penaeus vanamei  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T10495  
R:Sellos, D.Y.; van Wormhoudt, A.  
submitted to the EMBL Data Library, January 1997  
A:Description: Polymorphism of chymotrypsin gene sequences in the shrimp.  
A:Reference number: Z17057  
A:Accession: T10495  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-265 <SEL>  
A:Cross-references: EMBL:X10665  
C:Genetics:  
A:Note: Chymotrypsin B  
A:Note: Intron positions not resolved (incomplete sequence)  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 68.1%; Score 94; DB 2; Length 265;  
Best Local Similarity 68.0%; Pred. No. 8.6e-07;  
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
DB 40 IVGGTEAVPHSWPHQVALFIDCMYF 64

RESULT 3  
S61558  
chymotrypsin Pml - penaeid shrimp (Penaeus monodon) (fragment)  
C:Species: Penaeus monodon  
C:Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 16-Feb-1997  
C:Accession: S61558  
R:Tsal, I.H.; Lu, P.J.; Chuang, J.L.  
Biochim. Biophys. Acta 1080, 59-67, 1991  
A:Title: The midgut chymotrypsins of shrimps (Penaeus japonicus and Penaeus monodon), Penaeus japonicus and Penaeus monodon, PMID:1657178  
A:Reference number: S18356; MUID:92031652; PMID:1657178  
C:Accession: S61558  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-31 <TSA>  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: protein digestion

Query Match 65.9%; Score 91; DB 2; Length 31;  
Best Local Similarity 64.0%; Pred. No. 2.2e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
DB 1 IVGGVEAVPHSWPYQALFIIDMYF 25

RESULT 4  
KCUF  
brachyurin (EC 3.4.21.32) [validated] - Atlantic sand fiddler crab  
N:Alternate names: collagenolytic proteinase U  
C:Species: Uca pugnator (Atlantic sand fiddler crab)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 15-Sep-2000  
C:Accession: A00958  
R:Grant, G.A.; Henderson, K.O.; Eisen, A.Z.; Bradshaw, R.A.  
Biochemistry 19, 4653-4659, 1980  
A:Title: Amino acid sequence of a collagenolytic protease from the hepatopancreas of the fiddler crab, Uca pugnator, (Decapoda: Hippidae), PMID:6252953  
A:Reference number: A00958; MUID:81040004; PMID:6252953  
A:Accession: A00958  
A:Molecule type: protein  
A:Residues: 1-226 <GRA>  
Experimental source: tissue hepatopancreas  
R:Perona, J.J.; Fletterick, R.J.  
Submitted to the Brookhaven Protein Data Bank, November 1997  
A:Reference number: A73134; PDB:1A2Z  
A:Contents: annotation: X-ray crystallography, 2.3 angstroms, residues 1-90, 'I', 92-146, 'F';  
R:Perona, J.J.; Tsu, C.A.; Craik, C.S.; Fletterick, R.J.  
Biochemistry 36, 5381-5392, 1997  
A:Title: Crystal structure of an ecotin-collagenase complex suggests a model for recognition of collagen triple helix  
A:Reference number: A59231; MUID:97299771; PMID:9154920  
A:Contents: annotation: X-ray crystallography, 2.5 angstroms  
C:Complex: homodimer  
C:Function:  
A:Description: serine proteinase with a broad specificity, capable of degrading the native substrate, collagen  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: homodimer; hydrolase; protein degradation; protein digestion; serine proteinase  
F:1-218/Domain: trypsin homology <TRY>  
F:26-42,151-164,174-200/Disulfide bonds: #status experimental  
F:41,87,178/Active site: His, Asp, Ser #status predicted

Query Match 64.5%; Score 89; DB 1; Length 226;  
Best Local Similarity 64.0%; Pred. No. 4.2e-06;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25

DB 1 IVGGVEAVPNSPHQALFIDDMYF 25

RESULT 5  
S18356  
chymotrypsin (EC 3.4.21.1) Pm2 - penaeid shrimp (Penaeus monodon) (fragment)  
C:Species: Penaeus monodon  
C:Date: 22-Nov-1993 #sequence\_revision 01-Mar-1996 #text\_change 01-Nov-1996  
C:Accession: S18356  
R:Tsal, I.H.; Lu, P.J.; Chuang, J.L.  
Biochim. Biophys. Acta 1080, 59-67, 1991  
A:Title: The midgut chymotrypsins of shrimps (Penaeus monodon, Penaeus japonicus and Penaeus monodon), Penaeus japonicus and Penaeus monodon, PMID:1657178  
A:Reference number: S18356; MUID:92031652; PMID:1657178  
A:Accession: S18356  
A:Molecule type: protein  
A:Residues: 1-31 <TSA>  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 58.0%; Score 80; DB 2; Length 31;  
Best Local Similarity 60.0%; Pred. No. 1.1e-05;  
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
DB 1 IVGGVEAVPGVWPYQALFIIDMYF 25

RESULT 6  
B49878  
coagulation factor G beta chain precursor - horseshoe crab (Tachypleus tridentatus)  
C:Species: Tachypleus tridentatus  
C:Date: 30-Jun-1995 #sequence\_revision 30-Jun-1995 #text\_change 20-Jun-2000  
C:Accession: B49878  
R:Seki, N.; Muta, T.; Oda, T.; Iwaki, D.; Kuma, K.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 269, 1370-1374, 1994  
A:Title: Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A serine proteinase  
A:Reference number: A49878; MUID:94117453; PMID:8288603  
A:Accession: B49878  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-309 <SEK>  
A:Cross-references: GB:DI6623; NID:9459415; PIDN:BAA04045.1; PID:9459416  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hemolymph coagulation; heterodimer; serine proteinase; zymogen  
F:47-287/Domain: trypsin homology <TRY>

Query Match 53.6%; Score 74; DB 2; Length 309;  
Best Local Similarity 57.9%; Pred. No. 0.0012;  
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLF 19  
DB 47 IIGGGIATPHSPWPMVGF 65

RESULT 7  
A56900  
chymotrypsin I (EC 3.4.21.-) - penaeid shrimp (Penaeus vanamei) (fragment)  
C:Species: Penaeus vanamei  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Jun-2000  
C:Accession: A56900  
R:Van Wormhoudt, A.; Le Chevalier, P.; Sellios, D.  
Comp. Biochem. Physiol. B 103, 675-680, 1992  
A:Title: Purification, biochemical characterization and N-terminal sequence of a serine proteinase from the penaeid shrimp, Penaeus vanamei  
A:Reference number: A56900; MUID:93092601; PMID:1458841  
A:Accession: A56900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <VAN>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120229)

A:Note: a second variant, designated chymotrypsin II, had an identical N-terminal sequence.  
C:Comment: This enzyme has chymotrypsin and collagenolytic activities.  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 51.43; Score 71; DB 2; Length 20;  
Best Local Similarity 65.08; Pred. No. 0.00016;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFI 20  
|||||I|||:|||I  
DB 1 IVGGVEATPHSWPQRAALFI 20

## RESULT 8

A25528  
pancreatic elastase II (EC 3.4.21.71) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 22-Jun-1999  
Accession: A25528  
Ravenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.  
Biochim Biophys Acta 14, 8307-8330, 1986  
A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II gene  
A:Reference number: A93646; MUID:87066713; PMID:3641189  
A:Accession: A25528  
A:Molecule type: mRNA  
A:Residues: 1-271 <STE>  
A:Cross-references: GB:X04573; NID:g50825; PIDN:CAA28242.1; PID:g50826  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-271/Product: pancreatic elastase II #status predicted <MAT>  
F:31-264/Domain: trypsin homology <TRY>  
F:75,123,218/Active site: His, Asp, Ser #status predicted

Query Match 50.08; Score 69; DB 2; Length 271;  
Best Local Similarity 61.18; Pred. No. 0.006;  
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGL 18  
|||||I|||:||||I  
DB 31 VVGGOEATPTWNPQVSL 48

## RESULT 9

B61545  
plasmin (EC 3.4.21.7) precursor - sheep (fragments)  
N:Alternate names: miniplasminogen  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 28-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 17-Mar-1999  
C:Accession: B61545; S28200  
R:Schaller, J.; Rickli, E.E.  
Enzyme 40, 63-69, 1988  
A:Title: Structural aspects of the plasminogen of various species.  
A:Reference number: A61545; MUID:8905015; PMID:3168975  
A:Accession: B61545  
A:Molecule type: protein  
A:Residues: 1-37;38-117 <SCH>  
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.  
Protein Seq. Data Anal. 5, 21-25, 1992  
A:Title: Complete amino acid sequence of ovine miniplasminogen.  
A:Reference number: S28200; MUID:93149995; PMID:1492092  
A:Accession: S28200  
A:Molecule type: protein  
A:Residues: 118-460 <SC2>  
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; zymogen  
F:1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>  
F:1-37/Domain: activation peptide (fragment) #status experimental <APT>  
F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>  
F:41-118/Domain: kringle homology <KRA>  
F:118-460/Product: miniplasminogen #status experimental <MIN>

F:132-211/Domain: kringle homology <KR5>  
F:226-460/Domain: plasmin chain B #status experimental <BCH>  
F:231-453/Domain: trypsin homology <TRY>  
F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 50.08; Score 69; DB 2; Length 460;  
Best Local Similarity 61.18; Pred. No. 0.011;  
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGL 18  
|||||I|||:||||I  
DB 231 VVGCVATPHSWPQVSL 248

## RESULT 10

T30337  
polyprotein - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: T30337  
R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.  
submitted to the EMBL Data Library, March 1998  
A:Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from  
A:Reference number: Z20829  
A:Accession: T30337  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1524 <VAN>  
A:Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1

Query Match 50.08; Score 69; DB 2; Length 1524;  
Best Local Similarity 57.98; Pred. No. 0.042;  
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLF 19  
|||||I|||:||||I  
DB 584 IVGGEASPNWNPQVQIF 602

## RESULT 11

A23698  
trypsin (EC 3.4.21.59), skin - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 31-Oct-1997  
C:Accession: A23698  
R:Braganza, V.J.; Simmons, W.H.  
Biochemistry 30, 4997-5007, 1991  
A:Title: Trypsinase from rat skin: purification and properties.  
A:Reference number: A23698; MUID:91242400; PMID:2036367  
A:Accession: A23698  
A:Molecule type: protein  
A:Residues: 1-25 <BRA>  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase

Query Match 49.38; Score 68; DB 2; Length 25;  
Best Local Similarity 48.08; Pred. No. 0.00056;  
Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDIMYF 25  
|||||I|||:||||I  
DB 1 IVGGOEASGNKRPWQVSLRVXDITYW 25

## RESULT 12

PU0036  
serine proteinase (EC 3.4.21.-) - bovine (fragment)  
N:Alternate names: trypsin-like proteinase bPTLP  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 22-Apr-1995  
C:Accession: PU0036; PU0039  
R:Tsuji, A.; Sakiyama, K.; Edazawa, K.; Nagata, K.; Sasaki, Y.; Nagamune, H.; Matsuda  
submitted to JIPID, September 1994

RESULT 15  
S68825 pancreatic elastase (EC 3.4.21.36) isoform 1 precursor - human  
N:Alternate names: caldecrin isoform 1  
C:Species: Homo sapiens (man)  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 28-May-1999  
C:Accession: S68825  
R:Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura  
FEBS Lett. 386, 26-28, 1996  
A:Title: Molecular cloning and expression of human caldecrin.  
A:Reference number: S68825; MUID:96221765; PMID:8635596

RyTomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T.  
FEBS Lett. 386, 26-28, 1996

A>Title: Molecular cloning and expression of human caldesmon..  
A:Reference number: S68825; PMID:96221365; PMID:8635596

A:Accession: S68825

A;Molecule type: mRNA  
A:Residues: 1-268 <TOM>

A: Experimental source: pancreas  
C: Superfamily: trypsin; trypsin homology

C-Keywords: hydrolase; pancreas; serine proteinase; zymogen  
F1-16/Domain: signal sequence #status predicted <SIG>  
F17-29/Domain: propeptide #status predicted <PRO>  
F30-268/Product: pancreatic elastase isoform 1 #status predicted <MAT>  
F30-262/Domain: trypsin homology <TRY>

Query Match	48.6%	Score 67;	DB 2;	Length 268;
Best Local Similarity	50.0%;	Pred. No. 0.012;		
Matches 9;	Conservative	5;	Mismatches	4;
Indels	0;	Gaps	0;	

QY ~1 IVGGXEVTPHAYPNQVGL 18  
:||| : |||:| :  
Db 30 VVGGEDARPHSWPWISL 47

Search completed: May 30, 2005, 11:04:55  
Job time : 40 secs

Search completed: May 30, 2003, 11:04:55  
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 11:02:47 ; Search time 89 Seconds  
(without alignments)  
58.195 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGGXEVTPHAYPMQVGLFIDMYF 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 996614 seqs, 207175905 residues

1 number of hits satisfying chosen parameters: 996614

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	98.6	25	US-09-303-375A-1	Sequence 1, Appli
2	136	98.6	25	US-09-303-375A-2	Sequence 2, Appli
3	136	98.6	25	US-09-549-642-1	Sequence 1, Appli
4	136	98.6	25	US-09-549-642-2	Sequence 2, Appli
5	136	98.6	25	US-09-549-642-20	Sequence 20, Appli
6	136	98.6	300	US-09-644-022A-1	Sequence 1, Appli
7	101	73.2	25	US-09-644-022A-2	Sequence 2, Appli
8	101	73.2	25	US-09-303-375A-3	Sequence 3, Appli
9	101	73.2	25	US-09-549-642-3	Sequence 3, Appli
10	91	65.9	25	US-09-644-022A-6	Sequence 6, Appli
11	91	65.9	25	US-09-303-375A-7	Sequence 7, Appli
12	91	65.9	25	US-09-549-642-7	Sequence 7, Appli
13	89	64.5	25	US-09-644-022A-7	Sequence 7, Appli
14	89	64.5	25	US-09-303-375A-8	Sequence 8, Appli
15	89	64.5	25	US-09-549-642-8	Sequence 8, Appli
16	80	58.0	25	US-09-644-022A-5	Sequence 5, Appli
17	80	58.0	25	US-09-303-375A-6	Sequence 6, Appli
18	80	58.0	25	US-09-549-642-6	Sequence 6, Appli
19	75.5	54.7	287	PCT-US02-10780-130	Sequence 130, App
20	75.5	54.7	287	US-10-114-270-130	Sequence 130, App
21	75.5	54.7	602	US-60-452-680-23138	Sequence 23138, A
22	75.5	54.7	922	PCT-US02-10366-52	Sequence 52, Appli
23	75.5	54.7	932	US-10-363-937-6	Sequence 6, Appli
24	75.5	54.7	986	PCT-US02-10366-50	Sequence 50, Appli
25	70	50.7	273	US-10-219-051B-8824	Sequence 8824, A
26	70	50.7	273	US-10-219-051B-13255	Sequence 13255, A

27	70	50.7	273	6	US-10-219-051B-13259	Sequence 13259, A
28	68	49.3	20	5	US-09-644-022A-3	Sequence 3, Appli
29	68	49.3	20	5	US-09-303-375A-4	Sequence 4, Appli
30	68	49.3	20	5	US-09-303-375A-5	Sequence 5, Appli
31	68	49.3	20	5	US-09-549-642-4	Sequence 4, Appli
32	67	48.6	248	7	US-60-452-680-21123	Sequence 21123, A
33	67	48.6	248	7	US-60-453-135-12848	Sequence 12848, A
34	67	48.6	248	7	US-60-453-050-12848	Sequence 12848, A
35	67	48.6	268	6	US-10-405-027-3748	Sequence 3748, Ap
36	67	48.6	268	6	US-10-405-027-5294	Sequence 5294, Ap
37	67	48.6	268	7	US-60-452-680-21124	Sequence 21124, A
38	67	48.6	268	7	US-60-453-135-12849	Sequence 12849, A
39	67	48.6	268	7	US-60-453-050-12849	Sequence 12849, A
40	67	48.6	284	6	US-10-405-027-4680	Sequence 4680, Ap
41	67	48.6	433	5	US-09-949-016-8220	Sequence 8220, Ap
42	66	47.8	207	6	US-10-405-027-3476	Sequence 3476, Ap
43	66	47.8	207	6	US-10-405-027-4911	Sequence 4911, Ap
44	66	47.8	210	6	US-10-405-027-4909	Sequence 4909, Ap
45	66	47.8	260	1	PCT-US02-19297-125	Sequence 125, App

## ALIGNMENTS

RESULT 1  
US-09-303-375A-1  
; Sequence 1, Application US/09303375A  
; GENERAL INFORMATION:  
; APPLICANT: Johan R. de Faire  
; APPLICANT: Richard L. Franklin  
; APPLICANT: John Kay  
; APPLICANT: Ragnvald Lindblom  
; TITLE OF INVENTION: Multifunctional Enzyme  
; FILE REFERENCE: 314572-101E  
; CURRENT APPLICATION NUMBER: US/09/303,375A  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/385,540  
; PRIOR FILING DATE: 1995-02-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphausia superba  
US-09-303-375A-1

Query Match 98.6%; Score 136; DB 5; Length 25;  
Best Local Similarity 96.0%; Pred. No. 1.4e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGGXEVTPHAYPMQVGLFIDMYF 25  
DB 1 IVGGXEVTPHAYPMQVGLFIDMYF 25

RESULT 2  
US-09-303-375A-2  
; Sequence 2, Application US/09303375A  
; GENERAL INFORMATION:  
; APPLICANT: Johan R. de Faire  
; APPLICANT: Richard L. Franklin  
; APPLICANT: John Kay  
; APPLICANT: Ragnvald Lindblom  
; TITLE OF INVENTION: Multifunctional Enzyme  
; FILE REFERENCE: 314572-101E  
; CURRENT APPLICATION NUMBER: US/09/303,375A  
; CURRENT FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 08/486,820  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/385,540  
; PRIOR FILING DATE: 1995-02-08

```
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-303-375A-2

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4e-13;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 3
US-09-549-642-1
; Sequence 1, Application US/09549642
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: de Faire, Johan
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-549-642-1

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4e-13;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 4
US-09-549-642-2
; Sequence 2, Application US/09549642
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: de Faire, Johan
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-549-642-2

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4e-13;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 5
US-09-549-642-20
; Sequence 20, Application US/09549642
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: de Faire, Johan
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-549-642-20

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 6
US-09-644-022A-1
; Sequence 1, Application US/09644022A
; GENERAL INFORMATION:
; APPLICANT: Franklin, Richard L.
; APPLICANT: Cowling, Didier S.P.
; APPLICANT: Hubbel, Jeffrey A.
; APPLICANT: van de Wetering, Petra
```

```
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-549-642-2

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.4e-13;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGMEVTPHAYPWQVGLFIDDMYF 25

RESULT 5
US-09-549-642-20
; Sequence 20, Application US/09549642
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: de Faire, Johan
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphausia superba
; US-09-549-642-20

Query Match          98.6%; Score 136; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    |||| ||||||||||||||||||||
Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 6
US-09-644-022A-1
; Sequence 1, Application US/09644022A
; GENERAL INFORMATION:
; APPLICANT: Franklin, Richard L.
; APPLICANT: Cowling, Didier S.P.
; APPLICANT: Hubbel, Jeffrey A.
; APPLICANT: van de Wetering, Petra
```

;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 300  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-644-022A-1

Query Match 98.6%; Score 136; DB 5; Length 300;  
Best Local Similarity 96.0%; Pred. No. 1.7e-12;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 64 IVGGMEVTPHAYPWQVGLFIDDMYF 88

US-09-644-022A-2

;; Sequence 2, Application US/09644022A  
;; GENERAL INFORMATION:  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Cowling, Didier S.P.  
;; APPLICANT: Hubbel, Jeffrey A.  
;; APPLICANT: van de Wetering, Petra  
;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-644-022A-2

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPHQAALFIDDMYF 25

RESULT 8

US-09-303-375A-3  
;; Sequence 3, Application US/09303375A  
;; GENERAL INFORMATION:  
;; APPLICANT: Johan R. de Faire  
;; APPLICANT: Richard L. Franklin  
;; APPLICANT: John Kay  
;; APPLICANT: Ragnvald Lindblom  
;; TITLE OF INVENTION: Multifunctional Enzyme  
;; FILE REFERENCE: 314572-101E  
;; CURRENT APPLICATION NUMBER: US/09/303,375A  
;; CURRENT FILING DATE: 1999-04-30  
;; PRIOR APPLICATION NUMBER: US 08/486,820  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: US 08/385,540  
;; PRIOR FILING DATE: 1995-02-08  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-303-375A-3

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPHQAALFIDDMYF 25

RESULT 9

US-09-549-642-3  
;; Sequence 3, Application US/09549642  
;; GENERAL INFORMATION:  
;; APPLICANT: Phairson Medical, Inc.  
;; APPLICANT: de Faire, Johan  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Kay, John  
;; APPLICANT: Lindblom, Ragnvald  
;; TITLE OF INVENTION: Removing Dental Plaque with Krill  
;; FILE REFERENCE: 314572-101F  
;; CURRENT APPLICATION NUMBER: US/09/549,642  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 09/303,375  
;; PRIOR FILING DATE: 2000-04-30  
;; PRIOR APPLICATION NUMBER: 08/600,273  
;; PRIOR FILING DATE: 1996-02-08  
;; PRIOR APPLICATION NUMBER: 08/486,820  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: 08/385,540  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 3  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus vanamei  
US-09-549-642-3

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPHQAALFIDDMYF 25

RESULT 10

US-09-644-022A-6  
;; Sequence 6, Application US/09644022A  
;; GENERAL INFORMATION:  
;; APPLICANT: Franklin, Richard L.  
;; APPLICANT: Cowling, Didier S.P.  
;; APPLICANT: Hubbel, Jeffrey A.  
;; APPLICANT: van de Wetering, Petra  
;; TITLE OF INVENTION: Treatment of Trauma  
;; FILE REFERENCE: 314572-103B  
;; CURRENT APPLICATION NUMBER: US/09/644,022A  
;; CURRENT FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 25  
;; TYPE: PRP  
;; ORGANISM: Panaeus monodon chymotryptic  
US-09-644-022A-6

Query Match 65.9%; Score 91; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 1 IVGGVEAVPHSWPYQAALFIIDMYF 25

```

RESULT 13
US-09644-022A-7
  ; Sequence 7, Application US/09644022A
  ; GENERAL INFORMATION:
  ; APPLICANT: Franklin, Richard L.
  ; APPLICANT: Cowling, Didier S.P.
  ; APPLICANT: Hubbel, Jeffrey A.
  ; APPLICANT: van de Wetering, Petra
  ; TITLE OF INVENTION: Treatment of Trauma
  ; FILE REFERENCE: 314572-103B
  ; CURRENT APPLICATION NUMBER: US/09/644,022A
  ; CURRENT FILING DATE: 2000-08-23
  ; NUMBER OF SEQ ID NOS: 17
  ; SOFTWARE: FastSeq for Windows Version 4.0
  ; SEQ ID NO 7
  ; LENGTH: 25
  ; TYPE: PRT
  ; ORGANISM: Uca pugilator enzyme
US-09644-022A-7

```

Query Match 64.5%; Score 89; DB 5; Length 25;  
Best Local Similarity 64.0%; pred. No. 2e-06;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
||||| |:::| |||||  
Db 1 IVGGVEAVPNSWPQAAALFIDDMYF 25

```

RESULT 14
US-09-303-375A-8
: Sequence 8, Application US/09303375A
: GENERAL INFORMATION:
: APPLICANT: Johan R. de Faire
: APPLICANT: Richard L. Franklin
: APPLICANT: John Kay
: APPLICANT: Ragnvald Lindblom
: TITLE OF INVENTION: Multifunctional Enzyme
: FILE REFERENCE: 314572-101E
: CURRENT APPLICATION NUMBER: US/09/303,375A
: CURRENT FILING DATE: 1999-04-30
: PRIOR APPLICATION NUMBER: US 08/486,820
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: US 08/385,540
: PRIOR FILING DATE: 1995-02-08
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows version 4.0
: SEQ ID NO 8
: LENGTH: 25
: TYPE: PRT
: ORGANISM: Uca pugilator
US-09-303-375A-8

```

Query Match 64.5%; Score 89; DB 5; Length 25;  
Best Local Similarity 64.0%; pred. No. 2e-06;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
||||| | : : : | |||||  
Db 1 IVGGVEAVPNSWPQAAALFIDDMYF 25

RESULT 15  
US-09-549-642-8  
; Sequence 8, Application US/09549642  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: de Faire, Johan  
; APPLICANT: Franklin, Richard L.



```

; APPLICANT: Kay, John
; APPLICANT: Lindblom, Ragnvald
; TITLE OF INVENTION: Removing Dental Plaque with Krill
; TITLE OF INVENTION: Enzymes
; FILE REFERENCE: 314572-101F
; CURRENT APPLICATION NUMBER: US/09/549,642
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 09/303,375
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: 08/600,273
; PRIOR FILING DATE: 1996-02-08
; PRIOR APPLICATION NUMBER: 08/486,820
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/385,540
; PRIOR FILING DATE: 1995-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Uca pugilator
; 9-549-642-8

```

```

Query Match      64.5%; Score 89; DB 5; Length 25;
Best Local Similarity 64.0%; Pred. NO. 2e-06;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
       ||||| | |::| | |||||
Db      1 IVGGVEAVPNSWP HQAALFIDDMYF 25

```

Search completed: May 30, 2003, 11:12:20  
Job time : 89 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 11:01:13 ; Search time 26 Seconds  
(without alignments)  
28.291 Million cell updates/sec

Title: us-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGXEVTPHAYPMQVGLFIDDMYF 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pap:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pap:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pap:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pap:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pap:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	98.6	25	2	US-08-385-540A-1
2	136	98.6	25	2	US-08-385-540A-2
3	136	98.6	25	2	US-08-385-540A-17
4	136	98.6	25	2	US-08-600-273A-1
5	136	98.6	25	2	US-08-600-273A-2
6	136	98.6	25	2	US-08-600-273A-17
7	136	98.6	25	3	US-08-486-820-1
8	136	98.6	25	3	US-08-486-820-2
9	136	98.6	25	3	US-08-486-820-17
10	136	98.6	25	3	US-08-705-875A-19
11	136	98.6	25	4	US-09-220-731-1
12	136	98.6	25	4	US-09-220-731-2
13	136	98.6	25	4	US-09-220-731-20
14	136	98.6	178	3	US-08-705-875A-8
15	136	98.6	178	4	US-09-220-731-23
16	136	98.6	178	4	US-09-220-731-24
17	136	98.6	300	3	US-08-705-875A-4
18	136	98.6	300	3	US-08-705-875A-6
19	136	98.6	300	4	US-09-220-731-21
20	136	98.6	302	4	US-09-220-731-26
21	136	98.6	308	3	US-08-705-875A-10
22	123	89.1	23	4	US-09-220-731-19
23	101	73.2	25	2	US-08-385-540A-3
24	101	73.2	25	2	US-08-600-273A-3
25	101	73.2	25	3	US-08-486-820-3
26	101	73.2	25	4	US-09-220-731-3
27	96	69.6	211	4	US-09-220-731-25

Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 7, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 4, Appli  
Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-385-540A-1  
; Sequence 1, Application US/08385540A  
; Patent No. 5945102  
; GENERAL INFORMATION:  
; APPLICANT: de Faire, Johan  
; TITLE OF INVENTION: Wound Care With Multifunctional Enzyme  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/385.540A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/600.273  
; FILING DATE: 08-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 314572-101A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-385-540A-1

Query Match 98.6%; Score 136; DB 2; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 IVGXEVTPHAYPMQVGLFIDDMYF 25  
|||||

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

## RESULT 2

US-08-385-540A-2  
; Sequence 2, Application US/08385540A  
; Patent No. 5945102

## GENERAL INFORMATION:

APPLICANT: de Faire, Johan  
TITLE OF INVENTION: Wound Care With Multifunctional  
TITLE OF INVENTION: Enzyme  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads  
STREET: 997 Lenox Drive, Building 3, Suite 210  
CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,540A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/600,273

FILING DATE: 08-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-385-540A-2

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 96.0%; Pred. No. 3.5e-15;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

## RESULT 3

US-08-385-540A-17

; Sequence 17, Application US/08385540A

; Patent No. 5945102

## GENERAL INFORMATION:

APPLICANT: de Faire, Johan

TITLE OF INVENTION: Wound Care With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,540A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/600,273

FILING DATE: 08-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-385-540A-17

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

Db 1 IVGGNEVTPHAYPWQVGLFIDDMYF 25

## RESULT 4

US-08-600-273A-1

; Sequence 1, Application US/08600273A

; Patent No. 5958406

## GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-1

Query Match 98.6%; Score 136; DB 2; Length 25;

Best Local Similarity 96.0%; Pred. No. 3.5e-15;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGXVTPHAYPQVGLFIDDMYF 25

T 5

US-08-600-273A-2

Sequence 2, Application US/08600273A

Patent No. 5958406

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price &amp; Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-2

Query Match

Best Local Similarity 98.6%; Score 136; DB 2; Length 25;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGXVTPHAYPQVGLFIDDMYF 25

RESULT 6

US-08-600-273A-17

Sequence 17, Application US/08600273A

Patent No. 5958406

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Acne Treatment With Multifunctional

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price &amp; Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/600,273A

FILING DATE: 08-FEB-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/486,820

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/385,540

FILING DATE: 08-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 314572-101C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-600-273A-17

Query Match

Best Local Similarity 98.6%; Score 136; DB 2; Length 25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPQVGLFIDDMYF 25

Db 1 IVGGXVTPHAYPQVGLFIDDMYF 25

RESULT 7

US-08-486-820-1

Sequence 1, Application US/08486820

Patent No. 6030612

GENERAL INFORMATION:

APPLICANT: de Faire, Johan

APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John

TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486-820
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-101B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-820-2
;
; Query Match 98.6%; Score 136; DB 3; Length 25;
; Best Local Similarity 96.0%; Pred.No. 3.5e-15;
; Matches 24; Conservative. 0; Mismatches 1; Indels
;
QY 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25
;
; 11111111111111111111111111111111
;
DB 1 IVGGMEVTPHAYPMQVGLFIDDMYF 25
;
; 11111111111111111111111111111111
;
RESULT 9
US-08-486-820-17
; Sequence 17, Application US/08486820
; Patent No. 6030612
; GENERAL INFORMATION:
; APPLICANT: de Faire, Johan
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional
; TITLE OF INVENTION: Enzyme
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486-820
; FILING DATE:
; CLASSIFICATION: 424
;
US-08-486-820-17
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486-820
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-101B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-820-17

```

Query Match 98.6%; Score 136; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
|||||  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

## RESULT 10

US-08-705-875A-19  
; Sequence 19, Application US/08705875A  
; Patent No. 6040155  
; GENERAL INFORMATION:  
; APPLICANT: Kay, John  
; APPLICANT: Kille, Peter  
; TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING  
; TITLE OF INVENTION: SAME  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 997 Lenox Drive, Building 3, Suite 210  
; CITY: Lawrenceville  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08543  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/705,875A  
; FILING DATE: 28-AUG-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/768,318  
; FILING DATE: 17-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bloom, Allen  
; REGISTRATION NUMBER: 29,135  
; REFERENCE/DOCKET NUMBER: 314572-102US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-520-3214  
; TELEFAX: 609-520-3259  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-705-875A-19

Query Match 98.6%; Score 136; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
|||||  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

## RESULT 11

US-09-220-731-1  
; Sequence 1, Application US/09220731A  
; Patent No. 6232088  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: Richard L. Franklin  
; APPLICANT: Yves St. Pierre  
; TITLE OF INVENTION: Treatment and Prevention of Immune

; TITLE OF INVENTION: Rejection Reactions  
; FILE REFERENCE: 314572-101D  
; CURRENT APPLICATION NUMBER: US/09/220,731A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: PCT/SE93/00455  
; EARLIER FILING DATE: 1993-05-21  
; EARLIER APPLICATION NUMBER: 08/338,501  
; EARLIER FILING DATE: 1994-11-22  
; EARLIER APPLICATION NUMBER: 08/385,540  
; EARLIER FILING DATE: 1995-02-08  
; EARLIER APPLICATION NUMBER: 08/486,820  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/600,273  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphasia superba  
US-09-220-731-1

Query Match 98.6%; Score 136; DB 4; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
|||||  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

## RESULT 12

US-09-220-731-2  
; Sequence 2, Application US/09220731A  
; Patent No. 6232088  
; GENERAL INFORMATION:  
; APPLICANT: Phairson Medical, Inc.  
; APPLICANT: Richard L. Franklin  
; APPLICANT: Yves St. Pierre  
; TITLE OF INVENTION: Treatment and Prevention of Immune  
; TITLE OF INVENTION: Rejection Reactions  
; FILE REFERENCE: 314572-101D  
; CURRENT APPLICATION NUMBER: US/09/220,731A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: PCT/SE93/00455  
; EARLIER FILING DATE: 1993-05-21  
; EARLIER APPLICATION NUMBER: 08/338,501  
; EARLIER FILING DATE: 1994-11-22  
; EARLIER APPLICATION NUMBER: 08/385,540  
; EARLIER FILING DATE: 1995-02-08  
; EARLIER APPLICATION NUMBER: 08/486,820  
; EARLIER FILING DATE: 1995-06-07  
; EARLIER APPLICATION NUMBER: 08/600,273  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Euphasia superba  
US-09-220-731-2

Query Match 98.6%; Score 136; DB 4; Length 25;  
Best Local Similarity 96.0%; Pred. No. 3.5e-15;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
|||||  
Db 1 IVGGXVTPHAYPWQVGLFIDDMYF 25

## RESULT 13

US-09-220-731-20

```

; Sequence 20, Application US/09220731A
; Patent No. 6232088
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: Richard L. Franklin
; APPLICANT: Yves St. Pierre
; TITLE OF INVENTION: Treatment and Prevention of Immune
; REJECTION REACTIONS
; FILE REFERENCE: 314572-101D
; CURRENT APPLICATION NUMBER: US/09/220,731A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: PCT/SE93/00455
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 08/338,501
; EARLIER FILING DATE: 1994-11-22
; EARLIER APPLICATION NUMBER: 08/385,540
; EARLIER FILING DATE: 1995-02-08
; EARLIER APPLICATION NUMBER: 08/486,820
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/600,273
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Euphasia superba
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-220-731-20

```

```

Query Match          98.6%; Score 136; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
    |||||
Db 1 IVGGXVTPHAYPMQVGLFIDDMYF 25

```

```

RESULT 14
US-08-705-875A-8
; Sequence 8, Application US/08705875A
; Patent No. 6040155
; GENERAL INFORMATION:
; APPLICANT: Kay, John
; APPLICANT: Kille, Peter
; TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,875A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/768,318
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen

```

```

; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-102US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-705-875A-8

```

```

Query Match          98.6%; Score 136; DB 3; Length 178;
Best Local Similarity 96.0%; Pred. No. 3.3e-14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
    |||||
Db 72 IVGGXVTPHAYPMQVGLFIDDMYF 96

```

```

RESULT 15
US-09-220-731-23
; Sequence 23, Application US/09220731A
; Patent No. 6232088
; GENERAL INFORMATION:
; APPLICANT: Phairson Medical, Inc.
; APPLICANT: Richard L. Franklin
; APPLICANT: Yves St. Pierre
; TITLE OF INVENTION: Treatment and Prevention of Immune
; REJECTION REACTIONS
; FILE REFERENCE: 314572-101D
; CURRENT APPLICATION NUMBER: US/09/220,731A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: PCT/SE93/00455
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 08/338,501
; EARLIER FILING DATE: 1994-11-22
; EARLIER APPLICATION NUMBER: 08/385,540
; EARLIER FILING DATE: 1995-02-08
; EARLIER APPLICATION NUMBER: 08/486,820
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/600,273
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Euphasia
US-09-220-731-23

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Query Match          98.6%; Score 136; DB 4; Length 178;
Best Local Similarity 96.0%; Pred. No. 3.3e-14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 IVGGXVTPHAYPMQVGLFIDDMYF 25
    |||||
Db 72 IVGGXVTPHAYPMQVGLFIDDMYF 96

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Search completed: May 30, 2003, 11:05:29
Job time : 27 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 11:04:17 ; Search time 45 Seconds  
(without alignments)  
56.235 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 10123694 residues

number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	136	98.6	300	9	US-09-938-269-1
2	101	73.2	25	9	US-09-938-269-2
3	91	65.9	25	9	US-09-938-269-6
4	89	64.5	25	9	US-09-938-269-7
5	80	58.0	25	9	US-09-938-269-5
6	75.5	54.7	970	10	US-09-888-615-101
7	70	50.7	272	9	US-10-117-323-37
8	69	50.0	271	9	US-10-117-323-39
9	68	49.3	20	9	US-09-938-269-3
10	67	48.6	252	9	US-10-117-323-38
11	66	47.8	229	9	US-09-898-837A-53
12	66	47.8	260	9	US-09-978-295A-395
13	66	47.8	260	9	US-09-978-697-395
14	66	47.8	260	9	US-09-978-192A-395
15	66	47.8	260	9	US-09-999-832A-395
16	66	47.8	260	9	US-09-978-189-395
17	66	47.8	260	9	US-10-028-072-396
18	66	47.8	260	9	US-10-121-049-396
19	66	47.8	260	9	US-10-123-904-396

20	66	47.8	260	9	US-10-140-470-396	Sequence 396, App
21	66	47.8	260	9	US-10-175-746-396	Sequence 396, App
22	66	47.8	260	9	US-10-176-918-396	Sequence 396, App
23	66	47.8	260	9	US-10-176-921-396	Sequence 396, App
24	66	47.8	260	9	US-10-137-865-396	Sequence 396, App
25	66	47.8	260	9	US-10-140-474-396	Sequence 396, App
26	66	47.8	260	9	US-10-142-431-396	Sequence 396, App
27	66	47.8	260	9	US-10-143-114-396	Sequence 396, App
28	66	47.8	260	9	US-10-140-002-396	Sequence 396, App
29	66	47.8	260	9	US-09-978-608A-395	Sequence 395, App
30	66	47.8	260	9	US-10-142-419-396	Sequence 396, App
31	66	47.8	260	9	US-09-978-191A-395	Sequence 395, App
32	66	47.8	260	9	US-09-978-403A-395	Sequence 395, App
33	66	47.8	260	9	US-09-978-564A-395	Sequence 395, App
34	66	47.8	260	9	US-09-978-585A-395	Sequence 395, App
35	66	47.8	260	9	US-10-017-081A-395	Sequence 395, App
36	66	47.8	260	9	US-10-123-262-396	Sequence 396, App
37	66	47.8	260	9	US-10-142-423-396	Sequence 396, App
38	66	47.8	260	9	US-09-978-824-395	Sequence 395, App
39	66	47.8	260	9	US-09-981-915A-395	Sequence 395, App
40	66	47.8	260	9	US-09-999-833A-395	Sequence 395, App
41	66	47.8	260	9	US-10-121-050-396	Sequence 396, App
42	66	47.8	260	9	US-10-141-755-396	Sequence 396, App
43	66	47.8	260	9	US-10-167-749-395	Sequence 395, App
44	66	47.8	260	9	US-09-918-585A-395	Sequence 395, App
45	66	47.8	260	9	US-10-143-032-396	Sequence 396, App

ALIGNMENTS

RESULT 1

US-09-938-269-1  
: Sequence 1, Application US/09938269  
: Publication NO. US20030007951A1  
: GENERAL INFORMATION:  
: APPLICANT: Franklin, Richard L.  
: APPLICANT: Cowling, Didier S.P.  
: APPLICANT: Hubbel, Jeffrey A.  
: APPLICANT: van de Wetering, Petra  
: TITLE OF INVENTION: Treatment of Trauma  
: FILE REFERENCE: 314572-105  
: CURRENT APPLICATION NUMBER: US/09/938, 269  
: CURRENT FILING DATE: 2001-08-23  
: NUMBER OF SEQ ID NOS: 17  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: TYPE: PRT  
: ORGANISM: Panaeu vanameli  
US-09-938-269-1

Query Match 98.6%; Score 136; DB 9; Length 300;  
Best Local Similarity 96.0%; Pred. NO. 5.1e-13;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
|||||  
Db 64 IVGGMEVTPHAYPQVGLFIDDMYF 88

RESULT 2

US-09-938-269-2  
: Sequence 2, Application US/09938269  
: Publication NO. US20030007951A1  
: GENERAL INFORMATION:  
: APPLICANT: Franklin, Richard L.  
: APPLICANT: Cowling, Didier S.P.  
: APPLICANT: Hubbel, Jeffrey A.  
: APPLICANT: van de Wetering, Petra  
: TITLE OF INVENTION: Treatment of Trauma  
: FILE REFERENCE: 314572-105  
: CURRENT APPLICATION NUMBER: US/09/938, 269

Query Match  
Best Local Similarity 73.28; Score 101; DB 9; Length 25;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus vanamei  
US-09-938-269-2

Query Match  
Best Local Similarity 72.08; Score 101; DB 9; Length 25;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-6

Query Match  
Best Local Similarity 65.98; Score 91; DB 9; Length 25;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-6

Query Match  
Best Local Similarity 64.08; Score 91; DB 9; Length 25;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugnator enzyme  
US-09-938-269-7

Query Match  
Best Local Similarity 64.5%; Score 89; DB 9; Length 25;  
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugnator enzyme  
US-09-938-269-7

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-5

Query Match  
Best Local Similarity 58.08; Score 80; DB 9; Length 25;  
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-938-269-5

Query Match  
Best Local Similarity 54.78; Score 75.5; DB 10; Length 970;  
Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugnator enzyme  
US-09-938-269-7

Query Match  
Best Local Similarity 60.9%; Score 75.5; DB 10; Length 970;  
Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Query 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
Db 1 IVGGVEATPHSWPQAAALFIDDMYF 25  
SEQUENCE: 314572-105  
FILE REFERENCE: 314572-105  
CURRENT APPLICATION NUMBER: US/09/938,269  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugnator enzyme  
US-09-938-269-7

Query	Subject	Score	DB	Length	Indels	Gaps
Query Match	50.7%	Score 70;	DB 9;	Length 272;		
Best Local Similarity	48.0%	Pred. No. 0.0055;				
Matches	12;	Conservative	6;	Mismatches	7;	Indels
QY	1	IVGGXEVTPHAYPWQVGLFIDMYF	25			
DB	29	IVGGQEAQGNKWPQVSLRVNDTYW	53			
Query Match	50.0%	Score 69;	DB 9;	Length 271;		
Best Local Similarity	61.1%	Pred. No. 0.0077;				
Matches	11;	Conservative	3;	Mismatches	4;	Indels
QY	1	IVGGXEVTPHAYPWQVGL	18			
DB	31	VVGGQEAQTNTPWQVSL	48			
Query Match	50.0%	Score 69;	DB 9;	Length 271;		
Best Local Similarity	61.1%	Pred. No. 0.0077;				
Matches	11;	Conservative	3;	Mismatches	4;	Indels
QY	1	IVGGXEVTPHAYPWQVGL	18			
DB	31	VVGGQEAQTNTPWQVSL	48			

9-978-295A-395  
 Sequence 395, Application US/09978295A  
 Patent No. US202020156006A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnovers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Flivarov, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Geibert, Hanspeter  
 APPLICANT: Gritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: paoni, Nicholas F.  
 APPLICANT: ROY, Margaret Ann

PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-27  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084598  
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PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
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PRIOR APPLICATION NUMBER: 60/085323  
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PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.8%; Score 66; DB 9; Length 260;  
Best Local Similarity 52.6%; Pred. No. 0.021;  
Matches 10; Conservative 3; Mismatches 6; Indels 0; Caps 0;

QY 1 IVGGXEVTHAYPWQVGLF 19  
Db 33 VLGHECQPHSQPQAALF 51

RESULT 13

US-09-978-697-395  
Sequence 395, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2630P1C27  
 CURRENT APPLICATION NUMBER: US/09/978.697  
 CURRENT FILING DATE: 2001-10-16  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
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Query Match 47.8%; Score 66; DB 9; Length 260;

Best Local Similarity 52.6%; Pred. No. 0.021;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGKVTPTHPYQVGLF 19  
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 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
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 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630P1C9  
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 ; APPLICANT: Wood, William I.  
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 ; TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match      47.8%; Score 66; DB 9; Length 260;
Best Local Similarity 52.6%; Pred. NO. 0.021;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY      1 IVGGXEVTPHAYPWQVGLF 19
Db      33 VLGHECQPHSQPWQAALF 51

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Time : 46 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 10:50:27 ; Search time 22 Seconds  
(without alignments)  
47.132 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

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Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	70	50.7	273	1	P35002
6	69	50.0	271	1	P05208
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8	67	48.6	245	1	P81286
9	67	48.6	268	1	P80646
10	67	48.6	275	1	Q99895
11	66	47.8	260	1	Q92nd1
12	66	47.8	271	1	O60259
13	66	47.8	271	1	P00774
14	65	47.1	20	1	O15393
15	65	47.1	262	1	P34153
16	64	46.4	269	1	P12544
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24	63	45.7	812	1	P06868
25	63	45.7	1420	1	P20918
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DT	01-FEB-1994	(Rel. 28, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Chymotrypsin BI precursor (EC 3.4.21.1).			
OS	Penaeus vannamei (Penaeid shrimp) (European white shrimp).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;			
OC	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata;			
OC	Penaeoidea; Penaeidae; Litopenaeus.			
OX	NCBI_TaxID=6689;			
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RC	TISSUE=Hepatopancreas;			
RX	MEDLINE=92387359; PubMed=1516690;			
RA	Sellos D.; van Wormhoudt A.;			
RT	"Molecular cloning of a cDNA that encodes a serine protease with			
RT	chymotryptic and collagenolytic activities in the hepatopancreas of			
RT	the shrimp Penaeus vannamei (Crustacea, Decapoda).";			
RL	FEBS Lett. 309:219-224(1992).			
RN	[2]			
RP	SEQUENCE OF 46-65, AND CHARACTERIZATION.			
RC	TISSUE=Hepatopancreas;			
RX	MEDLINE=93092601; PubMed=1458841;			
RA	van Wormhoudt A.; le Chevalier P.; Sellos D.;			
RT	"Purification, biochemical characterization and N-terminal sequence			
RT	of a serine-protease with chymotryptic and collagenolytic activities			
RT	in a tropical shrimp, Penaeus vannamei (Crustacea, Decapoda).";			
RL	Comp. Biochem. Physiol. 103B:675-680(1992).			
CC	-1- FUNCTION: SERINE PROTEASE WITH CHYMOTRYPTIC AND COLLAGENOLYTIC			
CC	ACTIVITIES.			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa,			
CC	Phe-I-Xaa, Leu-I-Xaa.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-----			
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CC	-----			
DR	EMBL: X66415; CAA47046.1;			
DR	PIR: S22075; S22075.			
DR	PIR: S29239; S29239.			
DR	HSSP: P00771; IAZZ.			
DR	MEROPS: S01.121; -.			
DR	InterPro: IPR001314; Chymotrypsin.			
DR	InterPro: IPR001254; Ser-protease_Try.			
DR	Pfam: PF00089; trypsin; 1			
DR	PRINTS: PR00722; CHYMOTRYPSIN.			
DR	SMART: SM00020; Tryp-Spc; 1.			

## ALIGNMENTS

P50342 meriones un  
Q91iq8 mus musculu  
P06867 sus scrofa  
Q92r5 homo sapien  
Q61955 mus musculu  
O88780 rattus norv  
P28293 mus musculu  
P20151 homo sapien  
P47796 gadus morhu  
P08218 homo sapien  
Q29485 erinaceus e  
Q9ukq9 homo sapien

1 TRYT\_MERUN  
1 TMS2\_MOUSE  
1 PLMN\_PIG  
1 KLKF\_HUMAN  
1 NRPN\_MOUSE  
1 NRPN\_RAT  
1 CATG\_MOUSE  
1 KLK2\_HUMAN  
1 CTRA\_GADMO  
1 EL2B\_HUMAN  
1 PLMN\_ERIEU  
1 KLK9\_HUMAN

60 43.5 270 1  
35 60 43.5 490 1  
36 60 43.5 790 1  
37 59 42.8 256 1  
38 59 42.8 260 1  
39 59 42.8 260 1  
40 59 42.8 261 1  
41 59 42.8 261 1  
42 59 42.8 263 1  
43 59 42.8 269 1  
44 59 42.8 810 1  
45 58 42.0 250 1

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FT PROPEP      16 45      ACTIVATION PEPTIDE.
FT CHAIN       46 271    CHYMOTRYPSIN BII.
FT ACT_SITE    86      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE    86      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE    132     CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE    223     CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID    71 87    BY SIMILARITY.
FT DISULFID    196 209  BY SIMILARITY.
FT DISULFID    219 245  BY SIMILARITY.
SQ SEQUENCE    271 AA; 28723 MW; 2254D7C7E63FA2E1 CRC64;

Query Match      73.2%; Score 101; DB 1; Length 271;
Best Local Similarity 72.0%; Pred. No. 6e-08;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGSGEVTTHAYPWQVGLFDDMYF 25
   IIII IIII: I IIIIIII
Db 46 IVGSGEATPSNPHQAALFDDMYF 70

RESULT 3
COGS_UCAPU      STANDARD;      PRT; 226 AA.
ID COGS_UCAPU
AC P00771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Brachyurin (EC 3.4.21.32) (Collagenolytic protease).
OS Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae;
OC Uca complex; Celuca.
OX NCBI_TaxID=6772;
RN [1]
RP SEQUENCE.
RC TISSUE=Hepatopancreas;
RX MEDLINE=81040004; PubMed=6252953;
RA Grant G.A., Henderson K.O., Eisen A.Z., Bradshaw R.A.;
RT "Amino acid sequence of a collagenolytic protease from the
RT hepatopancreas of the fiddler crab, Uca pugnator.";
RRL Biochemistry 19:4653-4659(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).. AND REVISIONS.
RC TISSUE=Hepatopancreas;
RX MEDLINE=97299771; PubMed=9154920;
RA Perona J.J., Tsu C.A., Craik C.S., Fletterick R.J.;
RT "Crystal structure of an ecotin-collagenase complex suggests a model
RT for recognition and cleavage of the collagen triple helix.";
RRL Biochemistry 36:5381-5392(1997).
CC -!- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity
CC for peptide bonds, degrades native collagen at about 75% of the
CC length of the molecule from the N-terminus. Low activity on small
CC molecule substrates of both trypsin and chymotrypsin.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC PIR; A00958; KCUF.
CC PDB; 1AZZ; 25-FEB-98.
CC MEROPS; S01.122; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser.protease_Try.
DR Pfam; PF00889; trypsin; 1.
DR PRINTS; P00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Collagen degradation; 3D-structure.
FT ACT_SITE    41 41    CHARGE RELAY SYSTEM.
FT ACT_SITE    87 87    CHARGE RELAY SYSTEM.
FT ACT_SITE    178 178  CHARGE RELAY SYSTEM.
FT DISULFID    26 42
FT DISULFID    151 164

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FT DISULFID 174 200
FT CONFLICT 91 91
FT CONFLICT 147 148
FT CONFLICT 175 175
FT CONFLICT 185 185
FT CONFLICT 185 185
SQ SEQUENCE 226 AA; 23511 MW; 545591CAF332CE8C CRC64;

Query Match 64.5%; Score 89; DB 1; Length 226;
Best Local Similarity 64.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    ||||| 1:::1 | |||||
Db 1 IVGGVEAVPNSWPHQALFIDDMYF 25

RESULT 4
CTRP_PENMO
ID CTRP_PENMO STANDARD; PRT; 31 AA.
P35002;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin (EC 3.4.21.1) (Fragment).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata;
OC Penaeoidea; Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=92031652; PubMed=1657178;
RA Tsai I.H., Lu P.J., Chuang J.L.;
RT "The midgut chymotrypsins of shrimps (Penaeus monodon, Penaeus
japonicus and Penaeus penicillatus).";
RL Biochim. Biophys. Acta 1080:59-67(1991).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa,
Phe-I-Xaa, Leu-I-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR PIR: S18356; S18356.
DR HSP: P00771; 1A2Z.
DR MEROPS: S01.121; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
DR Hydrolase: Serine protease.
NON_TER 31
SQ SEQUENCE 31 AA; 3287 MW; 6CCDD09067D1D78 CRC64;

Query Match 58.0%; Score 80; DB 1; Length 31;
Best Local Similarity 60.0%; Pred. No. 9.8e-06;
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
    ||||| 1:::1 | |||||
Db 1 IVGGVEAVPNSWPHQALFIDDMYF 25

RESULT 5
MCT7_RAT
ID MCT7_RAT STANDARD; PRT; 273 AA.
AC P27435; P27435.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase,
DE skin).
GN MCT7 OR MCP7.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97149430; PubMed=8996238;
RA Lutzeltschwab C., Pejler G., Aveskog M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
different serine proteases and a carboxypeptidase A from various rat
mast cell populations.";
RL J. Exp. Med. 185:13-29(1997).
RN [2]
RN SEQUENCE OF 29-53.
RC STRAIN=Sprague-Dawley; TISSUE=SKIN;
RX MEDLINE=91242400; PubMed=2036367;
RA Braganza V.J., Simmons W.H.;
RT "Trypsin from rat skin: purification and properties.";
RL Biochemistry 30:4997-5007(1991).
RN [3]
RN SEQUENCE OF 29-51.
RC TISSUE=Breast carcinoma;
RX MEDLINE=92231826; PubMed=1314562;
RA Eto I., Grubbs C.J.;
RT "Separation, purification and N-terminal sequence analysis of a novel
leupeptin-sensitive serine endopeptidase present in chemically
induced rat mammary tumour.";
RL Biochem. J. 283:209-216(1992).
CC -1- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
RESPONSE OF THIS CELL TYPE.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-, Lys-I-, but
with more restricted specificity than trypsin.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
MAST CELL ACTIVATION.
CC -1- TISSUE SPECIFICITY: MAST CELLS.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: U67910; AAB48263.1; -.
DR PIR: A23698; A23698.
DR PIR: S21275; S21275.
DR HSP: P20231; 1AAO.
DR MEROPS: S01.026; -.
DR MEROPS: S01.143; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Serine protease; Glycoprotein; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 28 ACTIVATION PEPTIDE.
FT CHAIN 29 273 MAST CELL PROTEASE 7.
FT ACT_SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 57 73 BY SIMILARITY.
FT DISULFID 153 228 BY SIMILARITY.
FT DISULFID 186 209 BY SIMILARITY.

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FT DISULFID 218 246 BY SIMILARITY.  
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT CONFLICT 42 42 W -> V (IN REF. 3).  
 FT CONFLICT 49 51 NDT -> WLP (IN REF. 3).  
 SQ SEQUENCE 273 AA; 30400 MW; 65A5ED4D279FB284 CRC64;

Query Match 50.7%; Score 70; DB 1; Length 273;  
 Best Local Similarity 48.0%; Pred. No. 0.0027;  
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPNQVCLFDDMYF 25  
 ||||| : : : ||||| : : : || :  
 Db 29 IVGGQEAAGNKPQVSLRVNDYTW 53

RESULT 6  
 EL2\_MOUSE STANDARD; PRT; 271 AA.  
 ID EL2\_MOUSE  
 P05208;  
 13-AUG-1987 (Rel. 05, Created)  
 13-AUG-1987 (Rel. 05, Last sequence update)  
 15-JUN-2002 (Rel. 41, Last annotation update)  
 Elastase 2 precursor (EC 3.4.21.71).  
 GN ELA2.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=87066713; PubMed=3641189;  
 RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;  
 RT "Sequence organisation and transcriptional regulation of the mouse  
 elastase II and trypsin genes";  
 RL Nucleic Acids Res. 14:8307-8330(1986).  
 CC -1- FUNCTION: ACTS UPON ELASTIN.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-I-Xaa, Met-I-Xaa  
 and Phe-I-Xaa. Hydrolyzes elastin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.

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DR EMBL; X04573; CAA28242.1; .  
 DR EMBL; X04576; CAA28244.1; .  
 DR PIR; A25528; A25528.  
 DR HSP; P00772; IELG.  
 DR MEROPS; S01.155; .  
 DR MGD; MGI:95316; Ela2.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; trypsin; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Hydrolase; Serine protease; zymogen; Signal.  
 FT SIGNAL 1 16  
 FT PROPEP 17 30 ACTIVATION PEPTIDE.  
 FT CHAIN 31 271 ELASTASE 2.  
 FT ACT\_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 123 123 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 60 76 BY SIMILARITY.  
 FT DISULFID 157 224 BY SIMILARITY.

FT DISULFID 188 204 BY SIMILARITY.  
 FT DISULFID 214 245 BY SIMILARITY.  
 SQ SEQUENCE 271 AA; 28913 MW; FA542AE38FED3B4B CRC64;

Query Match 50.0%; Score 69; DB 1; Length 271;  
 Best Local Similarity 61.1%; Pred. No. 0.0037;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXVTPHAYPNQVGL 18  
 :||| : ||| : ||||| :  
 Db 31 VVGQEAATPNTWPQVSL 48

RESULT 7  
 PLMN\_SHEEP STANDARD; PRT; 343 AA.  
 ID PLMN\_SHEEP  
 AC P81286;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Plasminogen (EC 3.4.21.7) (Fragment).  
 GN PLG.  
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=93149995; PubMed=1492092;  
 RA Schaller J., Straub C., Kampfer U., Rickli E.E.;  
 RT "Complete amino acid sequence of ovine miniplasminogen";  
 RL Protein Seq. Data Anal. 5:21-25(1992).

CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS  
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING  
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,  
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE  
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN  
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH  
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,  
 LAMININ AND VON WILLEBRAND FACTOR.

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-I-Xaa > Arg-I-Xaa;  
 higher selectivity than trypsin. Converts fibrin into soluble  
 products.

CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN  
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO  
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN  
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.  
 HSSP; P00747; 5HPG.

DR MEROPS; S01.233; .

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001254; Ser\_protease\_Try.

DR Pfam; PF00051; kringle; 1.

DR Pfam; PF00089; trypsin; 1.

DR ProDom; PD000395; Kringle; 1.

DR SMART; SM00130; K8; 1.

DR SMART; SM00020; Tryp\_SPC; 1.

DR PROSITE; PS00021; KRINGLE\_1; 1.

DR PROSITE; PS00070; KRINGLE\_2; 1.

DR PROSITE; PS00240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; 1.

DR PROSITE; PS00135; TRYPSIN\_SER; 1.

KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;  
 Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.

FT NON\_TER 1 1

FT DOMAIN <1 140 HEAVY CHAIN A.

FT DOMAIN 141 >343 LIGHT CHAIN A.

FT DOMAIN <1 17 KRINGLE 4.

FT DOMAIN 41 120 KRINGLE 5.

FT DOMAIN 114 341 SERINE PROTEASE.

FT ACT\_SITE 181 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 224 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 319 CHARGE RELAY SYSTEM.  
 FT NON\_TER 343  
 SQ SEQUENCE 343 AA: 37662 MW; 8DF6EBA92D596EE0 CRC64;

Query Match 50.0%; Score 69; DB 1; Length 343;  
 Best Local Similarity 61.1%; Pred. No. 0.0047;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGXEVTPHAYPMQVGL 18  
 :111 111:11111  
 Db 114 VVGCVATPHSWPMQVSL 131

RESULT 8  
 CTRB\_GADMO  
 ID CTRB\_GADMO STANDARD; PRT; 245 AA.  
 AC P80646;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 Chymotrypsin B (EC 3.4.21.1).  
 GADMO morhua (Atlantic cod).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pyloric caeca;  
 RX MEDLINE=96439045; PubMed=8841380;  
 RA Leth-Larsen R., Asgerlsson B., Thorolfsson M., Noerregaard-Madsen M.,  
 RA Hoejrup P.;  
 RT "Structure of chymotrypsin variant B from Atlantic cod, Gadus  
 morhua.";  
 RL Biochim. Biophys. Acta 1297:49-56(1996).  
 RN [2]  
 RP SEQUENCE OF 1-12 AND 16-31.  
 RC TISSUE=Pyloric caeca;  
 RX MEDLINE=92111252; PubMed=1764912;  
 RA Asgerlsson B., Bjarnason J.B.;  
 RT "Structural and kinetic properties of chymotrypsin from Atlantic cod  
 (Gadus morhua). Comparison with bovine chymotrypsin.";  
 RL Comp. Biochem. Physiol. 99B:327-335(1991).  
 CC [1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-I-Xaa, Trp-I-Xaa,  
 Phe-I-Xaa, Leu-I-Xaa.  
 CC [1- SUBCELLULAR LOCATION: Extracellular.  
 CC [1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 HSSP: P00766; 1CHG.  
 MEROPS: S01.52; .

DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS02040; TRYPIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPIN\_SER; 1.  
 KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.  
 FT CHAIN 1 13  
 FT CHAIN 16 245  
 CHYMOTRYPSIN B, A CHAIN.  
 CHYMOTRYPSIN B, B CHAIN.  
 FT ACT\_SITE 57 57  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 101 101  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 195 195  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 1 121  
 BY SIMILARITY.  
 FT DISULFID 42 58  
 BY SIMILARITY.  
 FT DISULFID 135 201  
 BY SIMILARITY.  
 FT DISULFID 167 182  
 BY SIMILARITY.  
 FT DISULFID 191 220  
 BY SIMILARITY.  
 FT CONFLICT 9 11  
 QVT -> VIS (IN REF. 2).  
 FT CONFLICT 26 26  
 S -> T (IN REF. 2).  
 FT CONFLICT 28 29  
 PW -> Y (IN REF. 2).

SQ SEQUENCE 245 AA: 26260 MW; 74FE0D425517AB02 CRC64;  
 Query Match 48.6%; Score 67; DB 1; Length 245;  
 Best Local Similarity 61.1%; Pred. No. 0.0067;  
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IVGXEVTPHAYPMQVGL 18  
 :111 111:11111  
 Db 16 IVNGEAVPHSWPMQVSL 33

RESULT 9  
 CLCR\_HUMAN  
 ID CLCR\_HUMAN STANDARD; PRT; 268 AA.  
 AC Q99895; Q9NUH5; Q00765;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caldecrin precursor (EC 3.4.21.2) (Chymotrypsin C).  
 GN CTRC OR CLCR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANT TRP-80.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=96221265; PubMed=8635596;  
 RA Tomomura A., Akiyama M., Itoh H., Yoshino I., Tomomura M., Nishii Y.,  
 RA Nolkura T., Saheki T.;  
 RT "Molecular cloning and expression of human caldecrin.";  
 RL FEBS Lett. 386:26-28(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Coville G.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 17-268 FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Sziegoleit A.;  
 RT "A human pancreatic chymotrypsin: biochemical and molecular  
 characterization.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=98207038; PubMed=9538241;  
 RA Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,  
 RA Saheki T.;  
 RT "Caldecrin is a novel-type serine protease expressed in pancreas, but  
 its homologue, elastase IV, is an artifact during cloning derived  
 from caldecrin gene.";  
 RL J. Biochem. 123:546-554(1998).  
 CC [1- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC  
 ACTIVITY.  
 CC [1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-I-Xaa, Tyr-I-Xaa,  
 Phe-I-Xaa, Met-I-Xaa, Trp-I-Xaa, Glu-I-Xaa, Asn-I-Xaa.  
 CC [1- TISSUE SPECIFICITY: PANCREAS.  
 CC [1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; S82198; AAB47104.2; ALT\_SEQ.  
 DR EMBL; AL031283; CAB77355.1; .  
 DR EMBL; Y13697; CAA74031.1; .  
 DR HSSP: P00766; 1CHG.  
 DR MEROPS: S01.57; .  
 DR Genew; HGNC:2523; CTRC.

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DR MM: 601405;
DR InterPro: IPR001314; Chymotrypsin.
DR Pfam: PF00089; trypsin; 1
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPC; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW Polymorphism.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 29 ACTIVATION PEPTIDE.
FT CHAIN 30 268 CALDECRIN.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 216 216 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 17 141 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 222 BY SIMILARITY.
FT DISULFID 186 202 BY SIMILARITY.
FT DISULFID 212 243 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 80 80 R -> W.
FT CONFLICT 16 16 S -> T (IN REF. 1).
FT CONFLICT 52 52 N -> D (IN REF. 3).
SQ SEQUENCE 268 AA; 29484 MW; 460BF3B4A96516F CRC64;

Query Match 48.6%; Score 67; DB 1; Length 268;
Best Local Similarity 50.0%; Pred. No. 0.0073;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPQVGL 18
DB 30 VVGEDARHPWPQISL 47

RESULT 10
TRYTP_PIG
ID TRYTP_PIG STANDARD; PRT; 275 AA.
AC Q9N2D1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin precursor (EC 3.4.21.59).
DE MCTV.
DE Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20285343; PubMed=10824103;
RA Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,
RA Yano M., Yang B., Kido H.;
RT "Mast cell tryptase from pig lungs triggers infection by pneumotropic
RT Sendai and influenza A viruses. Purification and characterization."
RT Eur. J. Biochem. 267:3189-3197(2000).
CC -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
CC CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
CC RESPONSE OF THIS CELL TYPE.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC which more restricted specificity than trypsin.
CC -!- SUBUNIT: HOMOTETRAMER (By similarity).
CC -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
CC MAST CELL ACTIVATION.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC
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CC
CC EMBL; AB038652; BAA93614.1;
CC HSSP; P20231; IMAO.
CC MEROPS; S01.143;
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; TRYP-SPC; 1.
CC PROSITE; PS00240; TRYPsin_DOM; 1.
CC PROSITE; PS00134; TRYPsin_HIS; 1.
CC PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 31 275 TRYPTASE.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 275 AA; 30439 MW; ACC583647FCCB973 CRC64;

Query Match 48.6%; Score 67; DB 1; Length 275;
Best Local Similarity 52.0%; Pred. No. 0.0075;
Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPQVGLFIDDMYF 25
DB 31 IVGKEAPGCHKWPQVSLRCLDQYW 55

RESULT 11
KLK8_HUMAN
ID KLK8_HUMAN STANDARD; PRT; 260 AA.
AC O60259; Q9UQ47; Q9HCB3; Q9U1L9;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Neutrophin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
DE protease TADG-14) (Tumor-associated differentially expressed gene-14
DE protein).
DE GN
DE KLK8 OR PRSS19 OR TADG14 OR NRPN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=98372070; PubMed=9714609;
RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
RT "Sequence analysis and expression of human neutrophin CDNA and gene.";
RT Gene 213:9-16(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99203457; PubMed=10102990;
RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
RT "A novel form of human neutrophin, a brain-related serine protease, is
RT generated by alternative splicing and is expressed preferentially in
RT human adult brain.";
RT Eur. J. Biochem. 260:627-634(1999).

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SWART; SM00020; Tryp_SPC: 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HYDROLASE; Serine protease; Zymogen; Signal;
KW Alternative splicing.
FT SIGNAL; 1 28 POTENTIAL
FT PROPEP; 29 32 BY SIMILARITY.
FT CHAIN; 33 260 NEUROPSIN.
FT ACT_SITE; 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE; 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE; 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID; 39 173 BY SIMILARITY.
FT DISULFID; 58 74 BY SIMILARITY.
FT DISULFID; 145 246 BY SIMILARITY.
FT DISULFID; 152 218 BY SIMILARITY.
FT DISULFID; 184 198 BY SIMILARITY.
FT DISULFID; 208 233 BY SIMILARITY.
FT CARBOHYD; 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC; 23 23 A -> AACGSLDLLTKLYAENLPCVHLNPQWSPQSHCPRG
FT SQ SEQUENCE; 260 AA; 28048 MW; EF439E5B8C83E660 CRC64;
        WRSNLPAPAA (TN ISOPORM 2).

Query Match 47.8%; Score 66; DB 1; Length 260;
Best Local Similarity 52.6%; Pred. No. 0.01;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPWQVGLF 19
   :| | | | | :| | | |
DB 33 VLGGHECQPHSQPQAAFL 51

RESULT 12
EL2_RAT
ID EL2_RAT STANDARD; PRT; 271 AA.
AC P00774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Elastase 2 precursor (EC 3.4.21.71).
ELAA2.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82182957; PubMed=6918221;
RA McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L.,
RA Nikovits W., Rutter W.J.;
RT "Primary structure of two distinct rat pancreatic preproelastases
RT determined by sequence analysis of the complete cloned messenger
RT ribonucleic acid sequences.";
RL Biochemistry 21:1453-1463(1982).
RP [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=85054882; PubMed=6094548;
RA Swift G.H., Craik C.S., Stary S.J., Quinto C., Lahaie R.G.,
RA Rutter W.J., Macdonald R.J.;
RT "Structure of the two related elastase genes expressed in the rat
RT pancreas.";
RL J Biol Chem. 259:14271-14278(1984).
CC -1- FUNCTION: ACTS UPON ELASTIN.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa
CC and Phe-|-Xaa. Hydrolyzes elastin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY
CC -----
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CC EMBL; V01233; CAA24543.1; -
CC EMBL; L00124; AAA98780.1; -
CC EMBL; L00118; AAA98780.1; JOINED.
CC EMBL; L00119; AAA98780.1; JOINED.
CC EMBL; L00120; AAA98780.1; JOINED.
CC EMBL; L00121; AAA98780.1; JOINED.
CC EMBL; L00122; AAA98780.1; JOINED.
CC EMBL; L00123; AAA98780.1; JOINED.
CC PIR; A00961; ELRT2.
CC HSP; P00772; IELG.
CC MEROPS; S01.155; -
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30 ACTIVATION PEPTIDE.
FT CHAIN 31 271 ELASTASE 2.
FT ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 123 123 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 188 204 BY SIMILARITY.
FT DISULFID 214 245 BY SIMILARITY.
SQ SEQUENCE 271 AA; 28885 MW; 125C7839857B71E3 CRC64;

Query Match 47.8%; Score 66; DB 1; Length 271;
Best Local Similarity 55.6%; Pred. No. 0.01;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 IVGGXEVTHAYPWQVGL 18
    ||||| :|:::|||||
Db 31 VVGQEQASPNSWPQVSL 48

RESULT 13
TMS2_HUMAN STANDARD; PRT; 492 AA.
Q15393; Q9BXX1;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 2 precursor (EC 3.4.21.-).
GN TMPRSS2 OR PRSS10.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97468144; PubMed-9325052;
RA Antonarakis S.E.;
RT "Cloning of the TMPRSS2 gene, which encodes a novel serine protease
with transmembrane, LDLRA, and SRCR domains and maps to 21q22.3.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21309069; PubMed-11414763;
RA Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.;
RT "Mutation analyses of 268 candidate genes in human tumor cell lines.";
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RX MEDLINE-21139112; PubMed-11245484;
RA Afar D.E.H., Vivanco I., Hubert R.S., Kuo J., Chen E., Saffran D.C.,
RA Raitano A.B., Jakobovits A.;
RT "Catalytic cleavage of the androgen-regulated TMPRSS2 protease results
in its secretion by prostate and prostate cancer epithelia.";
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE-21104370; PubMed-11169526;
RA Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.T.;
RT "Expression of transmembrane serine protease TMPRSS2 in mouse and
human tissues.";
RN [5]
CC -i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED BY
CLEAVAGE AND SECRETED.
CC -i- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN SMALL INTESTINE. ALSO
EXPRESSED IN PROSTATE, COLON, STOMACH, AND SALIVARY GLAND.
CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -i- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
CC -i- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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FT DISULFID 172 231 BY SIMILARITY.  
 FT DISULFID 185 241 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 244 365 BY SIMILARITY.  
 FT DISULFID 281 297 BY SIMILARITY.  
 FT DISULFID 410 426 BY SIMILARITY.  
 FT DISULFID 437 465 BY SIMILARITY.  
 FT CARBOHYD 213 213 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT VARIANT 449 449 K -> N (IN DBSN:1056602).  
 FT MUTAGEN 255 255 /FTIQ-VAR\_011692.  
 FT MUTAGEN 441 441 R->O: LOSS OF CLEAVAGE.  
 FT CONFLICT 160 160 S->A: LOSS OF ACTIVITY.  
 FT CONFLICT 242 242 M -> V (IN REF. 3).  
 FT CONFLICT 329 329 I -> L (IN REF. 1).  
 FT CONFLICT 489 491 E -> O (IN REF. 1).  
 FT CONFLICT 489 491 RAD -> KAN (IN REF. 1).  
 SQ SEQUENCE 492 AA; 53891 MW; CAB44FD174A9076B CRC64;

Query Match 47.8%; Score 66; DB 1; Length 492;  
 Best Local Similarity 45.8%; Pred. No. 0.019;  
 Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

1 IVGGXEVTPHAYPWQVGLFIDMWY 24  
 |||| I I |||| I : : :  
 256 IVGGESALPGAPWQVSLHVQNVH 279

Db

RESULT 14  
 COG1\_CHIOP  
 ID COG1\_CHIOP STANDARD; PRT; 20 AA.  
 AC P34153;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Collagenolytic protease 25 kDa II/III (EC 3.4.21.32) (Fragment).  
 OS Chionoecetes opilio (Crab-beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;  
 OC Brachyura; Eubrachyura; Majoidae; Majidae; Chionoecetes.  
 OX NCBI\_TaxID=41210;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hepatopancreas;  
 RX MEDLINE=92120073; PubMed=1663026;  
 RA Kilnova O.A., Vedishcheva Y.V., Strongin A.Y.;  
 RT "Isolation and characteristics of collagenolytic enzymes from the  
 hepatopancreas of the crab Chionoecetes opilio.";  
 RL Dokl. Akad. Nauk SSSR 317:482-484(1991).  
 RL -!- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING  
 -!- THE NATIVE TRIPLE HELIX OF COLLAGEN.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity  
 for peptide bonds. Degrades native collagen at about 75% of the  
 length of the molecule from the N-terminus. Low activity on small  
 molecule substrates of both trypsin and chymotrypsin.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR MEROPS; S01.122;  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; PARTIAL.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; PARTIAL.  
 DR PROSITE; PS00135; TRYPSIN\_SER; PARTIAL.  
 KW Hydrolase; Serine protease; Collagen degradation.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2204 MW; C80D7B996E7281A7 CRC64;

Query Match 47.1%; Score 65; DB 1; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 0.0011;  
 Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 IVGGXEVTPHAYPWQVGLFI 20  
 |||| I |||| I ||||  
 1 IVGGQEA TPHTWVHQAVALFI 20

Db

RESULT 15  
 GRAA\_HUMAN  
 ID GRAA\_HUMAN STANDARD; PRT; 262 AA.  
 AC P12544;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Granzyme A precursor (EC 3.4.21.78) (Cytotoxic T-lymphocyte proteinase  
 1) (Hanukkah factor) (H factor) (HF) (Granzyme 1) (CTL tryptase)  
 DE (Fragmentin 1).  
 GN GZMA OR CTLA3 OR HFSP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=88125000; PubMed=3257574;  
 RA Gershenfeld H.K., Hershberger R.J., Shows T.B., Weissman I.L.;  
 RT "Cloning and chromosomal assignment of a human cDNA encoding a T  
 cell- and natural killer cell-specific trypsin-like serine  
 protease.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1184-1188(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RA Goralski T.J., Krensky A.M.;  
 RT "The upstream region of the human granzyme A locus contains both  
 positive and negative transcriptional regulatory elements.";  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 29-53.  
 RX MEDLINE=88330824; PubMed=30471119;  
 RA Poe M., Bennett C.D., Biddison W.E., Blake J.T., Norton G.P.,  
 RA Rodkey J.A., Sigal N.H., Turner R.V., Wu J.K., Zweerink H.J.;  
 RT "Human cytotoxic lymphocyte tryptase. Its purification from granules  
 and the characterization of inhibitor and substrate specificity.";  
 RL J. Biol. Chem. 263:13215-13222(1988).  
 RN [5]  
 RP SEQUENCE OF 29-40, AND CHARACTERIZATION.  
 RX MEDLINE=89009866; PubMed=3262682;  
 RA Hamed A., Lowrey D.M., Lichtenheld M., Podack E.R.;  
 RT "Characterization of three serine esterases isolated from human IL-2  
 activated killer cells.";  
 RL J. Immunol. 141:3142-3147(1988).  
 RN [6]  
 RP SEQUENCE OF 29-39, AND CHARACTERIZATION.  
 RX MEDLINE=89035468; PubMed=3263427;  
 RA Kraehenbuhl O., Rey C., Jenne D.E., Lanzavecchia A., Groscurth P.,  
 RA Carrel S., Tschopp J.;  
 RT "Characterization of granzymes A and B isolated from granules of  
 cloned human cytotoxic T lymphocytes.";  
 RL J. Immunol. 141:3471-3477(1988).  
 RN [7]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=89184501; PubMed=3237717;  
 RA Murphy M.E.P., Moulis J., Bleackley R.C., Gershenfeld H.,  
 RA Weissman I.L., James M.N.G.;  
 RT "Comparative molecular model building of two serine proteinases from  
 cytotoxic T lymphocytes.";  
 RL Proteins 4:190-204(1988).  
 CC -!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-  
 MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER LYS OR ARG. MAY BE  
 INVOLVED IN APOPTOSIS.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including fibronectin,  
 type IV collagen and nucleolin. Preferential cleavage: Arg-|-Xaa,  
 Lys-|-Xaa >> Phe-|-Xaa in small molecule substrates.  
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

-|- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES.  
 -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. GRANZYME SUBFAMILY.  
 -----  
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 -----  
 EMBL: M18737; AAA52647.1; -  
 EMBL: BC015739; AAH15739.1; -  
 EMBL: U40006; AAD00009.1; -  
 PIR: A28943; A28943.  
 PIR: A30525; A30525.  
 PIR: A30526; A30526.  
 PIR: A31372; A31372.  
 PDB: 1HF1; 15-OCT-94.  
 MEROPS: S01.135; -  
 Genew: HGNC:4708; GZMA.  
 MIM: 140050; -  
 InterPro: IPR001254; Ser\_protease\_Try.  
 Pfam: PF00089; trypsin; 1.  
 SMART: SM00020; Tryp\_SPC; 1.  
 PROSITE: PS0240; TRYPSIN\_DOM; 1.  
 PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 PROSITE: PS00135; TRYPSIN\_SER; 1.  
 Hydrolase: Serine protease; Zymogen; Signal; T-cell; Cytolysis;  
 Apoptosis; 3D-structure.  
 SIGNAL 1 26  
 PROPEP 27 28 ACTIVATION PEPTIDE.  
 CHAIN 29 262 GRANZYME A.  
 ACT\_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 ACT\_SITE 114 114 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 ACT\_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 DISULFID 54 70 BY SIMILARITY.  
 DISULFID 148 218 BY SIMILARITY.  
 DISULFID 179 197 BY SIMILARITY.  
 DISULFID 208 234 BY SIMILARITY.  
 CARBOHYD 170 170 N-LINKED (GLCNAC...) (POTENTIAL).  
 SEQUENCE 262 AA; 28968 MW; DA87363A0D92BAF4 CRC64;

Search completed: May 30, 2003, 11:02:43  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:57:47 ; Search time 79 Seconds  
(without alignments)  
65.205 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IGVGXEVTTPHAYPMQVGLFIDDMYF 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_21.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phase.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_rvrius.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	73.2	271	5	018487
2	95	68.8	270	5	08WR11
3	94	68.1	265	5	018488
4	89	64.5	270	5	Q27824
5	77	55.8	254	6	Q9XSN6
6	76	55.1	474	5	Q8T4N3
7	74	53.6	309	5	Q27083
8	72	52.2	255	11	Q9Z0M1
9	72	52.2	255	11	Q9JIS2
10	72	52.2	270	5	Q96871
11	71	51.4	465	5	Q9B3L7
12	69	50.0	467	5	Q967X8
13	69	50.0	868	5	Q9V1V3
14	69	50.0	1524	13	Q91674
15	67	48.6	263	13	Q9PWQ6
16	66	47.8	260	13	Q9W7Q3

17	66	47.8	269	11	Q9D7T9
18	66	47.8	269	11	Q9CQ52
19	66	47.8	492	4	Q9ET73
20	65	47.1	20	13	Q9PRR4
21	65	47.1	249	11	Q9QYN4
22	65	47.1	276	11	Q9QYN3
23	64	46.4	20	13	Q9PRR3
24	64	46.4	244	13	Q8QGW3
25	64	46.4	266	13	Q9W700
26	64	46.4	276	5	P91894
27	63	45.7	233	4	Q96RZ7
28	63	45.7	247	13	Q42158
29	63	45.7	247	13	Q42608
30	63	45.7	273	6	Q9XSM1
31	63	45.7	273	11	Q921N4
32	63	45.7	275	4	Q96RZ6
33	63	45.7	745	13	Q9PVY3
34	63	45.7	806	6	018783
35	63	45.7	812	11	Q9R0W3
36	63	45.7	812	11	Q91WJ5
37	62	44.9	159	4	Q96PT1
38	62	44.9	195	4	Q96PT0
39	62	44.9	244	13	Q42159
40	62	44.9	245	5	Q9BLI8
41	62	44.9	245	13	Q42160
42	62	44.9	246	5	Q9BLI7
43	62	44.9	282	5	Q25395
44	62	44.9	283	5	Q25394
45	62	44.9	283	5	Q95V22

ALIGNMENTS

RESULT 1

018487 O18487 PRELIMINARY; PRT; 271 AA.  
AC O18487;  
DC 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Chymotrypsin BI (Fragment).  
GN CHYMOTRYPSIN A.  
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Litopenaeus.  
OX NCBI\_TaxID=6689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPERMATOPHORUS;  
RX MEDLINE=99337490; PubMed=10407165;  
RA Sellos D.Y., Van Wormhoudt A.;  
RT "Polymorphism and evolution of collagenolytic serine protease genes in crustaceans";  
RL Biochim. Biophys. Acta 1432:419-424(1999).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.  
EMBL: Y10664; CAA71672.1; -.  
HSSP: P00771; IAZZ.  
DR MEROPS: S01.122; -.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR001254; Ser.protease\_Try.  
DR Pfam: PF00089; trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00020; TRYP\_SPC; 1.  
DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; Serine protease.  
FT NON\_TER 271 271  
SQ SEQUENCE 271 AA; 28743 MW; EAD3F41DD6053ADE CRC64;

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

Qy 1 IVGGXVTPHAYPWQVGLFIDDMYF 25  
 ||||| | : : : | | | | | | |  
 Db 45 IVGGVEAVPNSWPFOAALFIDDMYF 69

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RESULT 5
Q9XSN6 PRELIMINARY; PRT; 254 AA.
AC Q9XSN6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98126310; PubMed=9465170;
RA Simmer J.P., Fukae M., Tanabe T., Yamakoshi Y., Uchida T., Xue J.,
RA Margolis H.C., Shimizu M., DeHart B.C., Hu C.-C., Bartlett J.D.;
RA "Purification, characterization, and cloning of enamel matrix serine
proteinase 1.";
J. Dent. Res. 77:377-386(1998).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL; U76256; AAB94638.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.251; -.
DR InterPro; IPR001314; Chymotrypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 31 254 ENAMEL MATRIX SERINE PROTEINASE 1.
SQ SEQUENCE 254 AA; 27235 MW; FD40EF95664406F1 CRC64;

Query Match 55.8%; Score 77; DB 6; Length 254;
Best Local Similarity 44.0%; Pred. No. 0.0013;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDMYF 25
DB 31 IINGDCNPHSQPMQAALFLEDDFF 55

RESULT 6
Q8T4N3 PRELIMINARY; PRT; 474 AA.
AC Q8T4N3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Midgut serine proteinase-2.
OS Rhipicephalus appendiculatus (Brown ear tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=34631;
RN [1]
RP SEQUENCE FROM N.A.
RX Mulenga A., Onuma M., Sugimoto C.;
RA "Rhipicephalus appendiculatus midgut serine proteinase-2, cDNA cloning
and characterization.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078094; AAL79566.1; -.
SQ SEQUENCE 474 AA; 51232 MW; B01330E1F00EF49F CRC64;

Query Match 55.1%; Score 76; DB 5; Length 474;
Best Local Similarity 66.7%; Pred. No. 0.0036;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLFIDMYF 25
DB 31 IINGDCNPHSQPMQAALFLEDDFF 55

RESULT 7
Q27083 PRELIMINARY; PRT; 309 AA.
AC Q27083;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Clotting factor G beta subunit precursor.
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94117453; PubMed=8288603;
RA Seki N., Muta T., Oda T., Iwaki D., Kuma K., Miyata T., Iwanaga S.;
RA "Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A
serine protease zymogen heterodimer with similarities to beta-gluca-
binding proteins.";
J. Biol. Chem. 269:1370-1374(1994).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
CC EMBL; DL6623; BAA04045.1; -.
DR HSSP; P20231; IAAO.
DR MEROPS; S01.222; -.
DR InterPro; IPR001314; Chymotrypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 309 CLOTTING FACTOR G BETA SUBUNIT.
SQ SEQUENCE 309 AA; 34285 MW; 014F0B5F2BD56FDB CRC64;

Query Match 53.6%; Score 74; DB 5; Length 309;
Best Local Similarity 57.9%; Pred. No. 0.0046;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IVGGXEVTPHAYPMQVGLF 19
DB 47 IINGGIATPHSWPMVMGIF 65

RESULT 8
Q9Z0M1 PRELIMINARY; PRT; 255 AA.
AC Q9Z0M1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
GN K1K4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SWISS-WEBSTER;
RA Hu J.C.-C., Ryu O.H., Chen J.J., Uchida T., Wakida K., Murakami C.,
RA Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;
RA "Localization of EMS1 expression during tooth formation and cloning
```

of mouse cDNA.":  
RL J. Dent. Res. 79:70-76(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SWISS-WEBSTER:  
RX MEDLINE-20323211; PubMed-10863090;  
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;  
RT "Characterization of the mouse and human PRSS17 genes, their  
RT relationship to other serine proteases, and the expression of PRSS17  
RT in developing mouse incisors."  
RL Gene 251:1-8(2000).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; AF019979; AAC98894.1; -.  
DR HSSP; P00763; IDPO.  
DR MEROPS; S01.251; -.  
DR MGD; MGI:1861379; K1K4.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYSP-SPC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Serine protease; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 32 255 MATRIX SERINE PROTEINASE 1.  
SQ SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA0660A2A CRC64;  
Query Match 52.2%; Score 72; DB 11; Length 255;  
Best Local Similarity 44.0%; Pred. No. 0.0076;  
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
DB 32 IIQGDCSPHSQPWQAALFSEDGFF 56  
RESULT 9  
Q9JIS2  
ID Q9JIS2 PRELIMINARY; PRT; 255 AA.  
AC Q9JIS2  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Enamel matrix serine proteinase 1 precursor.  
DE KLK4 OR PRSS17.  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-129/SVJ;  
RX MEDLINE-20323211; PubMed-10863090;  
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;  
RT "Characterization of the mouse and human PRSS17 genes, their  
RT relationship to other serine proteases, and the expression of PRSS17  
RT in developing mouse incisors."  
RL Gene 251:1-8(2000).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; AF198031; AAF5937.1; -.  
DR HSSP; P00763; IDPO.  
DR MEROPS; S01.251; -.  
DR MGD; MGI:1861379; K1K4.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYSP-SPC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Serine protease; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 32 255 ENAMEL MATRIX SERINE PROTEINASE 1.  
FT VARIANT 15 15 Y -> C.  
FT VARIANT 251 251 T -> I.  
SQ SEQUENCE 255 AA; 27536 MW; CBF5FBAF7D4D679C CRC64;  
Query Match 52.2%; Score 72; DB 11; Length 255;  
Best Local Similarity 44.0%; Pred. No. 0.0076;  
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
QY 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
DB 32 IIQGDCSPHSQPWQAALFSEDGFF 56  
RESULT 10  
Q96871  
ID Q96871 PRELIMINARY; PRT; 270 AA.  
AC Q96871  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Serine proteinase.  
DE Trichinella spiralis.  
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;  
OC Trichinellidae; Trichinella.  
OX NCBI\_TaxID=6334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Todorova V., Xia Y., Moore J., Kennedy M.W.;  
RT "A CDNA encoding a stage-specific serine proteinase of Trichinella  
RT spiralis."  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
CC TRYPSIN FAMILY.  
DR EMBL; U62659; AAD09211.1; -.  
DR HSSP; P00763; IDPO.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYSP-SPC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyase; Serine protease.  
SQ SEQUENCE 270 AA; 28325 MW; 6E5233084FBB13B7 CRC64;  
Query Match 52.2%; Score 72; DB 5; Length 270;  
Best Local Similarity 60.0%; Pred. No. 0.008;  
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 IVGGXEVTPHAYPWQVGLFI 20  
DB 39 IVGGSDAVPSYPMQAHLSI 58  
RESULT 11  
Q9BJL7  
ID Q9BJL7 PRELIMINARY; PRT; 465 AA.  
AC Q9BJL7  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Newborn larvae-specific serine protease SS2.  
DE Trichinella spiralis.  
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;  
OC Trichinellidae; Trichinella.  
OX NCBI\_TaxID=6334;  
RN [1]



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RP SEQUENCE FROM N.A.
RC STRAIN-ISS 534;
RA Liu M., Li C., Garcia-Reyna P., Fu B., Roman T., Boireau P.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AF331160; AAK16520.1; -.
DR HSP; P00763; IDPO.
DR InterPro: IPR000875; Chymotrypsin.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00268; CECROPIN; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 465 AA; 50594 MW; 28B60795C5DA3EB1 CRC64;

Query Match 51.43; Score 71; DB 5; Length 465;
Best Local Similarity 61.13; Pred. No. 0.02;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGL 18
Db 82 IVGGTDVRPHSHPWQIQL 99

RESULT 12
Q967X8 PRELIMINARY; PRT; 467 AA.
AC Q967X8:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CUB-serine protease.
OS Panulirus argus (Spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Panuliridae; Panulirus.
OX NCBI_TaxID=6737;
RN SIGNAL 1
RP SEQUENCE FROM N.A.
RA Levine M.Z., Walthall W.W., Tai P.C., Derby C.D.;
RL "Molecular cloning, characterization, cellular localization and
possible function of a CUB-serine protease in the olfactory system of
the spiny lobster Panulirus argus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF357226; AAK48894.1; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
DR Hydrolase: Protease; Serine protease.
SQ SEQUENCE 467 AA; 50453 MW; 1D2E663D3314BBFD CRC64;

Query Match 50.08; Score 69; DB 5; Length 467;
Best Local Similarity 58.38; Pred. No. 0.039;
Matches 14; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFDDMY 24
Db 229 IVGGQETEVEVNEYPWQVLLVTRDMY 252

us-09-549-642-20.rspt
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RESULT 13
Q9Y1V3 PRELIMINARY; PRT; 868 AA.
AC Q9Y1V3:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tunicate retinoic acid-inducible modular protease precursor.
GN TRAMP.
OS Polyandrocarpa misakiensis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidacea;
OC Scolidobranchia; Styelidae; Polyandrocarpa.
OX NCBI_TaxID=7723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE SPOT;
RX MEDLINE=99423646; PubMed=10491255;
RA Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;
RL "A retinoic acid-inducible modular protease in budding ascidians.";
RL Dev. Biol. 214:38-45(1999).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: AB030007; BAA82522.1; -.
DR HSP; P00763; IDPO.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR001190; Srcr_receptor.
DR Pfam: PF00057; ldl_recept_a; 3.
DR Pfam: PF00530; SRCR; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00261; LDLRECEPTOR.
DR PRINTS: PR00258; SPERACTRCPTR.
DR SMART: SM00192; LDLa; 3.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; SR; 2.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS01209; LDLRA_1; 3.
DR PROSITE: PS0068; LDLRA_2; 3.
DR PROSITE: PS50287; SRCR_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1
SQ SEQUENCE 868 AA; 97660 MW; F71452865F36A6CA CRC64;

Query Match 50.08; Score 69; DB 5; Length 868;
Best Local Similarity 44.08; Pred. No. 0.074;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 IVGGXVTPHAYPMQVGLFDDMYF 25
Db 624 IVGGSGTEPHEWPMQAGIWLPTWY 648

RESULT 14
Q91674 PRELIMINARY; PRT; 1524 AA.
AC Q91674:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Polyprotein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
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